Application No.: 09/772116

Group Art Unit: 1639

AMENDMENTS TO THE CLAIMS

Please cancel claims 8 and 24-34, without prejudice, and amend claims 1, 9, 18, 19, 20, 22, and 23 as follows:

- 1. (Currently amended) A method for identifying a <u>non-peptide</u> compound that binds to a target, the method comprising:
 - a) forming a first library comprising a multiplicity of peptides;
 - b) selecting from the first library at least one peptide that binds to the target;
- c) determining the <u>amino acid</u> sequence or sequences of the at least one peptide that binds to the target, thereby generating a peptide motif;
- d) forming a second library comprising a multiplicity of non-peptide compounds designed based on the peptide motif;
- e) selecting from the second library at least one non-peptide compound that binds to the target; and
- f) determining the structure or structures of the at least one non-peptide compound that binds to the target;

thereby identifying a non-peptide compound that binds to the target.



- 2. (Original) The method of claim 1, wherein the first library is a phage display library.
- 3. (Original) The method of claim 1, wherein the first library is bound to a solid-support.
- 4. (Original) The method of claim 1, wherein the first library is an anchor library.
- 5. (Original) The method of claim 1, wherein the first library comprises at least about 10⁶ peptides.
- 6. (Original) The method of claim 1, wherein the first library comprises at least about 10⁹ peptides.
- 7. (Original) The method of claim 1, wherein the first library comprises at least about 10^{12} peptides.
- 8. (Canceled)

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9. (Original) The method of claim 1, wherein step c) comprises determining the amino acid sequence or sequences of the at least one peptide.

- 10. (Original) The method of claim 1, wherein the second library comprises at least one peptide derivative.
- 11. (Original) The method of claim 1, wherein the second library comprises at least one peptide analogue.
- 12. (Original) The method of claim 1, wherein the second library comprises at least one peptidomimetic.
- 13. (Original) The method of claim 1, wherein the second library comprises at least about 10^2 non-peptide compounds.
- 14. (Original) The method of claim 1, wherein the second library comprises at least about 10⁴ non-peptide compounds.
- 15. (Original) The method of claim 1, wherein the second library comprises at least about 10^6 non-peptide compounds.
- 16. (Original) The method of claim 1, wherein step f) comprises analyzing the at least one non-peptide compound by a mass spectrometric method.
- 17. (Original) The method of claim 16, wherein the mass spectrometric method comprises tandem mass spectrometry.
- 18. (Currently amended) The method of claim 1, wherein the <u>non-peptide</u> compound that binds to a target has a binding affinity for the target of at least about 10⁻⁷ M.
- 19. (Currently amended) The method of claim 1, wherein the <u>non-peptide</u> compound that binds to a target has a binding affinity for the target of at least about 10^{-8} M.
- 20. (Currently amended) The method of claim 1, wherein the <u>non-peptide</u> compound that binds to a target has a binding affinity for the target of at least about 10^{-9} M.

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21. (Original) The method of claim 1, further comprising:

- g) forming a third library comprising a multiplicity of non-peptide compounds designed based on the structure or structures of the non-peptide compound or compounds determined in step f);
- h) selecting from the third library at least one non-peptide compound that binds to the target; and
- i) determining the structure or structures of the at least one non-peptide compound selected in step h);

thereby identifying a compound that binds to the target.

- 22. (Currently amended) A method for identifying a <u>non-peptide</u> compound that binds to a target, the method comprising:
- a) forming a first library comprising a multiplicity of peptides displayed on the surface of a bacteriophage;
 - b) selecting from the first library at least one peptide that binds to the target;
- c) determining the sequence or sequences of the at least one peptide that binds to the target, thereby generating a peptide motif;
- d) forming a second library comprising a multiplicity of non-peptide compounds designed based on the peptide motif;
- e) selecting from the second library at least one non-peptide compound that binds to the target; and
- f) determining the structure or structures of the at least one non-peptide compound that binds to the target by tandem mass spectrometry;

thereby identifying a non-peptide compound that binds to the target.

- 23. (Currently amended) A method for identifying a <u>non-peptide</u> compound that binds to a target, the method comprising:
 - a) forming a first library comprising an anchor library of a multiplicity of peptides;
 - b) selecting from the first library at least one peptide that binds to the target;
- c) determining the sequence or sequences of the at least one peptide that binds to the Target, thereby generating a peptide motif;
- d) forming a second library comprising a multiplicity of non-peptide compounds designed based on the peptide motif;
- e) selecting from the second library at least one non-peptide compound that binds to the target; and



f) determining the structure or structures of the at least one non-peptide compound that binds to the target by tandem mass spectrometry;

thereby identifying a <u>non-peptide</u> compound that binds to the target.

- 24. (Canceled)
- 25. (Canceled)
- 26. (Canceled)
- 27. (Canceled)
- 28. (Canceled)
- 29. (Canceled)
- 30. (Canceled)
- 31. (Canceled)
- 32. (Canceled)
- 33. (Canceled)
- 34. (Canceled)